



PCT10

ENTERED

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/009,823A

DATE: 03/19/2003
 TIME: 14:20:51

Input Set : A:\DAVIE150SEQLIST.TXT
 Output Set: N:\CRF4\03192003\J009823A.raw

4 <110> APPLICANT: Panaccio, Michael
 5 Rosey, Everett Lee
 6 Sinistaj, Meri
 7 Hasse, Detlef
 8 Parsons, Jim
 9 Ankenbauer, Robert G.
 11 <120> TITLE OF INVENTION: LAWSONIA DERIVED GENE AND RELATED FLGE
 12 POLYPEPTIDES, PEPTIDES AND PROTEINS AND THEIR USES
 15 <130> FILE REFERENCE: DAVI150.001APC
 17 <140> CURRENT APPLICATION NUMBER: US 10/009,823A
 C--> 18 <141> CURRENT FILING DATE: 2002-08-13
 20 <150> PRIOR APPLICATION NUMBER: PCT/AU00/00437
 21 <151> PRIOR FILING DATE: 2000-05-11
 23 <150> PRIOR APPLICATION NUMBER: US 60/133,973
 24 <151> PRIOR FILING DATE: 1999-05-13
 26 <160> NUMBER OF SEQ ID NOS: 13
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 502
 32 <212> TYPE: PRT
 33 <213> ORGANISM: Lawsonia intracellularis
 35 <400> SEQUENCE: 1
 36 Met Met Gly Ser Leu Phe Ile Gly Ala Thr Gly Met Lys Thr His Ser
 37 1 5 10 15
 38 Thr Gly Leu Gly Thr Val Ser Asn Asn Ile Ala Asn Ala Asn Thr Ile
 39 20 25 30
 40 Gly Tyr Lys Gln Gln Gln Val Val Phe Gln Asp Leu Phe Ser Gln Asp
 41 35 40 45
 42 Leu Ala Ile Gly Ser Thr Gly Ser Gln Gly Pro Asn Gln Ala Gly Met
 43 50 55 60
 44 Gly Ala Gln Val Gly Ser Val Arg Thr Ile Phe Thr Gln Gly Ala Phe
 45 65 70 75 80
 46 Glu Pro Gly Asn Ser Val Thr Asp Leu Ala Ile Gly Gly Lys Gly Phe
 47 85 90 95
 48 Phe Gln Val Thr Leu Glu Asp Lys Val His Tyr Thr Arg Ala Gly Asn
 49 100 105 110
 50 Phe Arg Phe Thr Gln Asp Gly Phe Leu Asn Asp Pro Ser Gly Phe Thr
 51 115 120 125
 52 Leu Met Gly Ser Arg Ile Ser Asn Asn Pro Asn Ile Lys Lys Glu Thr
 53 130 135 140
 54 Leu Glu Pro Ile Gln Leu Asp Phe Asn Asp Pro Thr Val Ala Lys Ser
 55 145 150 155 160
 56 Pro Ala Lys Thr Ser Thr Ala Leu Asn Ala Val Val Asn Leu Gly Asp

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57	165	170	175
58	Ser Thr Asp Lys Thr Gln Ser Glu Ala Asn Pro Tyr Phe Ala Leu Leu		
59	180	185	190
60	Glu Ser Trp Lys Gly Asn Gly Thr Pro Pro Ile Ser Thr Ser Asn Tyr		
61	195	200	205
62	Ser Tyr Ala Gln Pro Met Arg Val Tyr Asp Gln Gln Gly Asn Ser His		
63	210	215	220
64	Asp Ile Thr Val Tyr Phe Asp Gly Ala Pro Ser Ser Thr Gly Ser Lys		
65	225	230	235
66	240	245	250
67	255	260	265
68	270	275	280
69	285	290	295
70	300	305	310
71	315	320	325
72	335	340	345
73	350	355	360
74	365	370	375
75	380	385	390
76	400	405	410
77	415	420	425
78	430	435	440
79	445	450	455
80	460	465	470
81	475	480	490
82	495	500	
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102	<210> SEQ ID NO: 2		
103	<211> LENGTH: 1509		
104	<212> TYPE: DNA		
105	<213> ORGANISM: Lawsonia intracellularis		
107	<400> SEQUENCE: 2		
108	atgatgggaa gtttgtttat tggtgcaaca ggtatgaaaa cccatagtagc agggttgggt 60		

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109 actgtctcca ataatattgc taacgcaa at accattgggt ataagcagca acaggtagtg 120
 110 tttcaagacc tgtttagtca agat tagca ataggttcta ctggaa gggccaa ac 180
 111 caggctggta tgggagcaca gtttggaa gttcgacaa tttttacaca gggtgcttt 240
 112 gaacctggca atagtgtaac agat cttgtc attggtaggaa aagg ttttt tcaggttaca 300
 113 ttagaggata aagtacacta tacacgagca gggat tttc gttttactca agatggttt 360
 114 ttaaatgatc ctacggatt tacttaatg ggctcaagaa tatctaataa tccta acata 420
 115 aaaaaggaaa cccttgaacc aattcagta gacttaatg atcctacagt agcaaagtct 480
 116 cctgc aaaa caagtacagc attaaacgct gtggtaa acc ttggtagt tacagataaa 540
 117 acacaaagtg aagctaatcc atactttgca cttctt gaga gctggaaagg aaatggaaca 600
 118 cctccttattt ctacatcaaa ctactcatat gcacaaccta tgagagtata t gatcaacaa 660
 119 gggaaattctc acgatataac tttatattt gatggagcac cctcttcaac aggaagtaaa 720
 120 acatttgaat acctttagc tatgaatcct agtgaagatg gaagtgctc atcaggaaca 780
 121 gatagtgcag gtctttaat gtctggaa act atgacattt caagtaatgg cgaattaaaa 840
 122 aatatgacag ctttactcc tactggctc gcaacaaaag atttaatgc atggcaacca 900
 123 gcaccattag tcaatggttt accacagttt tcagcaattt ttgttgggc aggaatacag 960
 124 ctttaacat tagacttgg aattaaaagc caacagaata tttgggcagg agtccagca 1020
 125 tccgctgctg ccataggtac agatattggg aatttgcattt caatgatgcc aatacaaaaca 1080
 126 tccagcggta attctacagc aagaaatgca tcatttca caagaagata tagccaagat 1140
 127 gtttacatcctc agggagatct agtagatgtc acaatttacat ctgaaaggaa attacaaggt 1200
 128 aagtatagta atagtcagg ttttattt tataatattt ctttagcactt ctttacaagt 1260
 129 gaggatggat taagacgaga agggaaataac cattattccg caacacttga ctcaggtagg 1320
 130 ccagagttt gattgccagg aacatctaa tatgaaaac ttatgtgaa tcaacttgag 1380
 131 acttctaacg tagacatgag cagagaaatg gttaatatga ttattattca acgtggttt 1440
 132 cagatgaata gtaaatctgt tacaacagca gacacaatgc tacaacaaaagc acttgaacta 1500
 133 aagcgttaa 1509
 135 <210> SEQ ID NO: 3
 136 <211> LENGTH: 21
 137 <212> TYPE: DNA
 138 <213> ORGANISM: Artificial Sequence
 140 <220> FEATURE:
 141 <223> OTHER INFORMATION: Oligonucleotide primer, RA170.
 143 <400> SEQUENCE: 3
 144 ctat ttttag gagatgttat c 21
 146 <210> SEQ ID NO: 4
 147 <211> LENGTH: 22
 148 <212> TYPE: DNA
 149 <213> ORGANISM: Artificial Sequence
 151 <220> FEATURE:
 152 <223> OTHER INFORMATION: Oligonucleotide primer, RA171.
 154 <400> SEQUENCE: 4
 155 tacaacaaat acaataaaat ac 22
 157 <210> SEQ ID NO: 5
 158 <211> LENGTH: 38
 159 <212> TYPE: DNA
 160 <213> ORGANISM: Artificial Sequence
 162 <220> FEATURE:
 163 <223> OTHER INFORMATION: Oligonucleotide primer, FlaF.
 W--> 165 <221> NAME/KEY: misc_feature
 166 <222> LOCATION: (1)...(38)

RAW SEQUENCE LISTING
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Input Set : A:\DAVIE150SEQLIST.TXT
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167 <223> OTHER INFORMATION: n = A,T,C or G
W--> 169 <400> 5
W--> 170 gcgaaattcca tatgatgggg agtttgttta ttgntgcc 38
172 <210> SEQ ID NO: 6
173 <211> LENGTH: 40
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Oligonucleotide primer, FlgE3'.
180 <400> SEQUENCE: 6
181 gctctagaga ctatgttat taacgcttta gttcaagtgc 40
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 477
185 <212> TYPE: PRT
186 <213> ORGANISM: Treponema phagedenis
188 <400> SEQUENCE: 7
189 Met Met Arg Ser Leu Phe Ser Gly Val Ser Gly Met Gln Asn His Gln
190 1 5 10 15
191 Gly Val Asn Pro Lys Glu Val Gly Leu Gly Val Met Val Ala Ser Gly
192 20 25 30
193 Val Asn Pro Lys Glu Val Gly Leu Gly Val Met Val Ala Ser Thr Arg
194 35 40 45
195 Met Asp Val Ile Gly Asn Asn Val Ala Asn Val Asn Thr Thr Gly Phe
196 50 55 60
197 Lys Arg Gly Arg Ile Asp Thr Val His Thr Gln Gly Ala Leu Gln Thr
198 65 70 75 80
199 Thr Gly Ile Asn Thr Asp Ile Ala Ile Val Asn Phe Gln Asp Leu Ile
200 85 90 95
201 Ser Gln Gln Leu Ser Gly Ala Ser Arg Pro Asn Glu Glu Val Gly Gln
202 100 105 110
203 Gly Asn Gly Phe Phe Ile Leu Lys Asp Gly Glu Lys Ser Phe Tyr Thr
204 115 120 125
205 Thr Ala Gly Ala Phe Gly Val Asp Arg Asp Gly Thr Leu Val Asn Pro
206 130 135 140
207 Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Val Gln Gly
208 145 150 155 160
209 Trp Met Ala Glu Asp Ile Glu Gly Gln Ile Ile Asn Thr Ser Asp
210 165 170 175
211 Gln Pro Glu Leu Pro Glu Gly Ala Asn Gln Ala Asp Ile Leu Arg Ser
212 180 185 190
213 Thr Glu Asp Leu Ile Ile Pro Ile Gly Gln Lys Ile Asp Ala Lys Ala
214 195 200 205
215 Thr Thr Asp Val Ala Tyr Thr Trp Ala Thr Asp Phe Asn Val Tyr Asp
216 210 215 220
217 Thr Phe Gly Glu Gln His Lys Leu Gln Met Val Phe Ser Arg Val Pro
218 225 230 235 240
219 Gly Thr Asn Asn Gln Trp Leu Ala Thr Val Val Thr Asp Thr Ala Gly
220 245 250 255
221 Asn Val Thr Ala Pro Asn Val Asp Pro Glu Asn Gln Ala Gly Thr Glu

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222	260	265	270
223	Thr Arg Val Gly Ile Gly Thr Thr Asp Gly Ala Gly Gln Val Leu Val		
224	275	280	285
225	Gln Ala Thr Glu Asn Thr Phe Ile Val Ser Phe Asp Asn Tyr Gly His		
226	290	295	300
227	Leu Ala Ser Ser Tyr Asn Val Val Gly Ala Asn Pro Asp Glu Gly Gly		
228	305	310	315
229	Ala Pro Thr Arg His Thr Phe Asn Ile Asn Asp Gln Ser Gly Ile Ile		
230	325	330	335
231	Thr Gly Val Tyr Ser Asn Gly Ala Ser Leu Glu Gly Glu Ile Gly Thr		
232	340	345	350
233	Ser Arg Asn Thr Ile Thr Gln Phe Ala Glu Arg Glu Ile Gly Gln Leu		
234	355	360	365
235	Ala Leu Ala Gly Phe Ala Asn Gln Gly Gly Leu Glu Lys Ala Gly Glu		
236	370	375	380
237	Ser Thr Thr Lys Ala Tyr Gln Gln Asp Gly Tyr Ala Met Gly Tyr Leu		
238	385	390	395
239	Glu Asn Phe Lys Ile Thr Tyr Ile Gln Ser Asn Asn Ser Gly Ile Ala		
240	405	410	415
241	Asn Ile Thr Val Ser Gly Val Met Gly Lys Gly Lys Leu Ile Ala Gly		
242	420	425	430
243	Thr Leu Glu Met Ser Asn Val Asp Leu Thr Asp Gln Phe Thr Asp Met		
244	435	440	445
245	Ile Ile Thr Gln Arg Gly Phe Gln Ala Gly Ala Lys Thr Ile Gln Thr		
246	450	455	460
247	Ser Asp Thr Met Leu Glu Thr Val Leu Asn Leu Lys Arg		
248	465	470	475
251	<210> SEQ ID NO: 8		
252	<211> LENGTH: 462		
253	<212> TYPE: PRT		
254	<213> ORGANISM: Treponema pallidum		
256	<400> SEQUENCE: 8		
257	Met Met Arg Ser Leu Phe Ser Gly Val Ser Gly Met Gln Asn His Gln		
258	1	5	10
			15
259	Gly Val Asn Pro Lys Glu Val Gly Leu Gly Val Leu Ile Ala Ser Thr		
260	20	25	30
261	Arg Met Asp Val Ile Gly Asn Asn Val Ala Asn Val Asn Thr Thr Gly		
262	35	40	45
263	Phe Lys Arg Gly Arg Ile Asp Thr Val His Thr Gln Gly Ala Leu Gln		
264	50	55	60
265	Thr Thr Gly Ile Asn Thr Asp Val Ser Ile Val Asn Phe Gln Asp Leu		
266	65	70	75
			80
267	Ile Ser Gln Gln Leu Ser Ala Ala Ala Arg Pro Asn Glu Glu Val Gly		
268	85	90	95
269	Gln Gly Ser Gly Phe Phe Val Leu Lys Ser Gly Glu Lys Thr Phe Phe		
270	100	105	110
271	Thr Arg Ala Gly Ala Phe Gly Val Asp Asn Ala Gly Thr Leu Val Asn		
272	115	120	125
273	Pro Ala Asn Gly Ala Cys Asn Leu Asp Lys Arg Leu Met Arg Val Gln		

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 34

Seq#:10; Xaa Pos. 197

VERIFICATION SUMMARY

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Input Set : A:\DAVIE150SEQLIST.TXT

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L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:165 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:169 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:192